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# 2



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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/078,059

DATE: 03/05/2002 P5  
 TIME: 14:12:03

Input Set : A:\PF466P2SEQLIST01102002.txt  
 Output Set: N:\CRF3\03052002\J078059.raw

3 <110> APPLICANT: Ruben et al.  
 5 <120> TITLE OF INVENTION: Cytokine Receptor Common Gamma Chain Like  
 7 <130> FILE REFERENCE: PF466P2  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/078,059  
 C--> 9 <141> CURRENT FILING DATE: 2002-02-20  
 9 <150> PRIOR APPLICATION NUMBER: 60/269,876  
 10 <151> PRIOR FILING DATE: 2001-02-21  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US00/22493  
 13 <151> PRIOR FILING DATE: 2000-08-17  
 15 <150> PRIOR APPLICATION NUMBER: 09/376,430  
 16 <151> PRIOR FILING DATE: 1999-08-18  
 18 <150> PRIOR APPLICATION NUMBER: 09/263,626  
 19 <151> PRIOR FILING DATE: 1999-03-05  
 21 <150> PRIOR APPLICATION NUMBER: PCT/US99/05068  
 22 <151> PRIOR FILING DATE: 1999-03-05  
 24 <150> PRIOR APPLICATION NUMBER: 60/086,505  
 25 <151> PRIOR FILING DATE: 1998-05-22  
 27 <150> PRIOR APPLICATION NUMBER: 60/078,563  
 28 <151> PRIOR FILING DATE: 1998-03-19  
 30 <160> NUMBER OF SEQ ID NOS: 32  
 32 <170> SOFTWARE: PatentIn Ver. 2.1  
 34 <210> SEQ ID NO: 1  
 35 <211> LENGTH: 1573  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Homo sapiens  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: CDS  
 41 <222> LOCATION: (13)..(1125)  
 43 <400> SEQUENCE: 1  
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 45 Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe  
 46 1 5 10  
 48 ctg ctg gga ggc tgg atg gct ttg ggg caa gga gca gca gaa gga 99  
 49 Leu Leu Gly Gly Trp Met Ala Leu Gly Gln Gly Ala Ala Glu Gly  
 50 15 20 25  
 52 gta cag att cag atc atc tac ttc aat tta gaa acc gtg cag gtg aca 147  
 53 Val Gln Ile Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr  
 54 30 35 40 45  
 56 tgg aat gcc agc aaa tac tcc agg acc aac ctg act ttc cac tac aga 195  
 57 Trp Asn Ala Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg  
 58 50 55 60  
 60 ttc aac ggt gat gag gcc tat gac cag tgc acc aac tac ctt ctc cag 243  
 61 Phe Asn Gly Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln

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62	65	70	75	
64	gaa ggt cac act tcg ggg tgc ctc cta gac gca gag cag cga gac gac			291
65	Glu Gly His Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp			
66	80	85	90	
68	att ctc tat ttc tcc atc agg aat ggg acg cac ccc gtt ttc acc gca			339
69	Ile Leu Tyr Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala			
70	95	100	105	
72	agt cgc tgg atg gtt tat tac ctg aaa ccc agt tcc ccg aag cac gtg			387
73	Ser Arg Trp Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val			
74	110	115	120	125
76	aga ttt tcg tgg cat cag gat gca gtg acg gtg acg tgt tct gac ctg			435
77	Arg Phe Ser Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu			
78	130	135	140	
80	tcc tac ggg gat ctc ctc tat gag gtt cag tac ccg agc ccc ttc gac			483
81	Ser Tyr Gly Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp			
82	145	150	155	
84	acc gag tgg cag tcc aaa cag gaa aat acc tgc aac gtc acc ata gaa			531
85	Thr Glu Trp Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu			
86	160	165	170	
88	ggc ttg gat gcc gag aag tgt tac tct ttc tgg gtc agg gtg aag gct			579
89	Gly Leu Asp Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala			
90	175	180	185	
92	atg gag gat gta tat ggg cca gac aca tac cca agc gac tgg tca gag			627
93	Met Glu Asp Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu			
94	190	195	200	205
96	gtg aca tgc tgg cag aga ggc gag att ccg gat gcc tgt gca gag aca			675
97	Val Thr Cys Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr			
98	210	215	220	
100	cca acg cct ccc aaa cca aag ctg tcc aaa ttt att tta att tcc agc			723
101	Pro Thr Pro Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser			
102	225	230	235	
104	ctg gcc atc ctt ctg atg gtg tct ctc ctt ctg tct tta tgg aaa			771
105	Leu Ala Ile Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys			
106	240	245	250	
108	tta tgg aga gtg aag aag ttt ctc att ccc agc gtg cca gac ccg aaa			819
109	Leu Trp Arg Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys			
110	255	260	265	
112	tcc atc ttc ccc ggg ctc ttt gag ata cac caa ggg aac ttc cag gag			867
113	Ser Ile Phe Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu			
114	270	275	280	285
116	tgg atc aca gac acc cag aac gtg gcc cac ctc cac aag atg gca ggt			915
117	Trp Ile Thr Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly			
118	290	295	300	
120	gca gag caa gaa agt ggc ccc gag gag ccc ctg gta gtc cag ttg gcc			963
121	Ala Glu Gln Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala			
122	305	310	315	
124	aag act gaa gcc gag tct ccc agg atg ctg gac cca cag acc gag gag			1011
125	Lys Thr Glu Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu			
126	320	325	330	

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128 aaa gag gcc tct ggg gga tcc ctc cag ctt ccc cac cag ccc ctc caa 1059  
 129 Lys Glu Ala Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln  
 130 335 340 345  
 132 ggc ggt gat gtg gtc aca atc ggg ggc ttc acc ttt gtg atg aat gac 1107  
 133 Gly Gly Asp Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp  
 134 350 355 360 365  
 136 cgc tcc tac gtg gcg ttg tgatggacac accactgtca aagtcaacgt 1155  
 137 Arg Ser Tyr Val Ala Leu  
 138 370  
 140 caggatcoac gttgacattt aaagacagag gggactgtcc cggggactcc acaccaccat 1215  
 142 ggatggaaag tctccacgcc aatgatgta ggacttaggactctgaaga cccagcctca 1275  
 144 cccgcctaattg cggccactgc cctgctaact ttccccaca tgagtcttg tgttcaaagg 1335  
 146 ctgtatggca gatgggagcc aattgttcca ggagatttac tcccagttcc ttttcgtgcc 1395  
 148 tgaacgttgtt cacataaacc ccaaggcagc acgtccaaaa tgctgtaaaa ccatcttccc 1455  
 150 actctgtgag tccccagttc cgtccatgtc cctgttccat agcattggat tctcggagga 1515  
 152 tttttgtct gtttgagac tccaaaccac ctctaccctt aaaaaaaaaa aaaaaaaaaa 1573  
 155 <210> SEQ ID NO: 2  
 156 <211> LENGTH: 371  
 157 <212> TYPE: PRT  
 158 <213> ORGANISM: Homo sapiens  
 160 <400> SEQUENCE: 2  
 161 Met Gly Arg Leu Val Leu Leu Trp Gly Ala Ala Val Phe Leu Leu Gly  
 162 1 5 10 15  
 164 Gly Trp Met Ala Leu Gly Gln Gly Ala Ala Glu Gly Val Gln Ile  
 165 20 25 30  
 167 Gln Ile Ile Tyr Phe Asn Leu Glu Thr Val Gln Val Thr Trp Asn Ala  
 168 35 40 45  
 170 Ser Lys Tyr Ser Arg Thr Asn Leu Thr Phe His Tyr Arg Phe Asn Gly  
 171 50 55 60  
 173 Asp Glu Ala Tyr Asp Gln Cys Thr Asn Tyr Leu Leu Gln Glu Gly His  
 174 65 70 75 80  
 176 Thr Ser Gly Cys Leu Leu Asp Ala Glu Gln Arg Asp Asp Ile Leu Tyr  
 177 85 90 95  
 179 Phe Ser Ile Arg Asn Gly Thr His Pro Val Phe Thr Ala Ser Arg Trp  
 180 100 105 110  
 182 Met Val Tyr Tyr Leu Lys Pro Ser Ser Pro Lys His Val Arg Phe Ser  
 183 115 120 125  
 185 Trp His Gln Asp Ala Val Thr Val Thr Cys Ser Asp Leu Ser Tyr Gly  
 186 130 135 140  
 188 Asp Leu Leu Tyr Glu Val Gln Tyr Arg Ser Pro Phe Asp Thr Glu Trp  
 189 145 150 155 160  
 191 Gln Ser Lys Gln Glu Asn Thr Cys Asn Val Thr Ile Glu Gly Leu Asp  
 192 165 170 175  
 194 Ala Glu Lys Cys Tyr Ser Phe Trp Val Arg Val Lys Ala Met Glu Asp  
 195 180 185 190  
 197 Val Tyr Gly Pro Asp Thr Tyr Pro Ser Asp Trp Ser Glu Val Thr Cys  
 198 195 200 205  
 200 Trp Gln Arg Gly Glu Ile Arg Asp Ala Cys Ala Glu Thr Pro Thr Pro  
 201 210 215 220

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203 Pro Lys Pro Lys Leu Ser Lys Phe Ile Leu Ile Ser Ser Leu Ala Ile  
 204 225 230 235 240  
 206 Leu Leu Met Val Ser Leu Leu Leu Ser Leu Trp Lys Leu Trp Arg  
 207 245 250 255  
 209 Val Lys Lys Phe Leu Ile Pro Ser Val Pro Asp Pro Lys Ser Ile Phe  
 210 260 265 270  
 212 Pro Gly Leu Phe Glu Ile His Gln Gly Asn Phe Gln Glu Trp Ile Thr  
 213 275 280 285  
 215 Asp Thr Gln Asn Val Ala His Leu His Lys Met Ala Gly Ala Glu Gln  
 216 290 295 300  
 218 Glu Ser Gly Pro Glu Glu Pro Leu Val Val Gln Leu Ala Lys Thr Glu  
 219 305 310 315 320  
 221 Ala Glu Ser Pro Arg Met Leu Asp Pro Gln Thr Glu Glu Lys Glu Ala  
 222 325 330 335  
 224 Ser Gly Gly Ser Leu Gln Leu Pro His Gln Pro Leu Gln Gly Gly Asp  
 225 340 345 350  
 227 Val Val Thr Ile Gly Gly Phe Thr Phe Val Met Asn Asp Arg Ser Tyr  
 228 355 360 365  
 230 Val Ala Leu  
 231 370  
 235 <210> SEQ ID NO: 3  
 236 <211> LENGTH: 379  
 237 <212> TYPE: PRT  
 238 <213> ORGANISM: Homo sapiens  
 240 <400> SEQUENCE: 3  
 241 Met Leu Lys Pro Pro Leu Pro Leu Arg Ser Leu Leu Phe Leu Gln Leu  
 242 1 5 10 15  
 244 Pro Leu Leu Gly Val Gly Leu Asn Pro Lys Phe Leu Thr Pro Ser Gly  
 245 20 25 30  
 247 Asn Glu Asp Ile Gly Gly Lys Pro Gly Thr Gly Gly Asp Phe Phe Leu  
 248 35 40 45  
 250 Thr Ser Thr Pro Ala Gly Thr Leu Asp Val Ser Thr Leu Pro Leu Pro  
 251 50 55 60  
 253 Lys Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met Asn Cys Thr Trp  
 254 65 70 75 80  
 256 Asn Ser Ser Ser Glu Pro Gln Pro Asn Asn Leu Thr Leu His Tyr Gly  
 257 85 90 95  
 259 Tyr Arg Asn Phe Asn Gly Asp Asp Lys Leu Gln Glu Cys Gly His Tyr  
 260 100 105 110  
 262 Leu Phe Ser Glu Gly Ile Thr Ser Gly Cys Trp Phe Gly Lys Lys Glu  
 263 115 120 125  
 265 Ile Arg Leu Tyr Glu Thr Phe Val Val Gln Leu Gln Asp Pro Arg Glu  
 266 130 135 140  
 268 His Arg Lys Gln Pro Lys Gln Met Leu Lys Leu Gln Asp Leu Val Ile  
 269 145 150 155 160  
 271 Pro Trp Ala Pro Glu Asn Leu Thr Leu Arg Asn Leu Ser Glu Phe Gln  
 272 165 170 175  
 274 Leu Glu Leu Ser Trp Ser Asn Arg Tyr Leu Asp His Cys Leu Glu His  
 275 180 185 190

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Input Set : A:\PF466P2SEQLIST01102002.txt  
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277 Leu Val Gln Tyr Arg Ser Asp Arg Asp Arg Ser Trp Thr Glu Gln Ser  
278 195 200 205  
280 Val Asp His Arg His Ser Phe Ser Leu Pro Ser Val Asp Ala Gln Lys  
281 210 215 220  
283 Leu Tyr Thr Phe Arg Val Arg Ser Arg Tyr Asn Pro Leu Cys Gly Ser  
284 225 230 235 240  
286 Ala Gln His Trp Ser Asp Trp Ser Tyr Pro Ile His Trp Gly Ser Asn  
287 245 250 255  
289 Thr Ser Lys Glu Asn Ile Glu Asn Pro Glu Asn Pro Ser Leu Phe Ala  
290 260 265 270  
292 Leu Glu Ala Val Leu Ile Pro Leu Gly Ser Met Gly Leu Ile Val Ser  
293 275 280 285  
295 Leu Ile Cys Val Tyr Cys Trp Leu Glu Arg Thr Met Pro Arg Ile Pro  
296 290 295 300  
298 Thr Leu Lys Asn Leu Glu Asp Leu Val Thr Glu Tyr Gln Gly Asn Phe  
299 305 310 315 320  
301 Ser Ala Trp Ser Gly Val Ser Lys Gly Leu Ala Glu Ser Leu Gln Pro  
302 325 330 335  
304 Asp Tyr Ser Glu Arg Leu Cys His Val Ser Glu Ile Pro Pro Lys Gly  
305 340 345 350  
307 Gly Glu Gly Pro Gly Gly Ser Pro Cys Ser Gln His Ser Pro Tyr Trp  
308 355 360 365  
310 Ala Pro Pro Cys Tyr Thr Leu Lys Pro Glu Pro  
311 370 375  
314 <210> SEQ ID NO: 4  
315 <211> LENGTH: 733  
316 <212> TYPE: DNA  
317 <213> ORGANISM: Homo sapiens  
319 <400> SEQUENCE: 4  
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321 aattcgagggt tgcacccgtca gtcttcctt tccccccaaa accccaaggac accctcatga 120  
322 tctcccgacatc tccgtggatc acatgcgtgg tgggtggacgt aagccacgaa gaccctgagg 180  
323 tcaagttcaa ctggtaacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240  
324 aggagcgtta caacacgacg taccgtgtgg tcagcgtctt caccgtctg caccaggact 300  
325 ggctgaatgg caaggagtac aagtgcagg tctccaacaa agccctccca acccccattcg 360  
326 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420  
327 catcccgaa tgagctgacc aagaaccagg tcagcctgac ctgcctgtc aaaggcttct 480  
328 atccaagcga catgccgtg gagtgggaga gcaatggca gccggagaac aactacaaga 540  
329 ccacgcctcc cgtgctggac tccgacggct ccttcttctt ctacagcaag ctcaccgtgg 600  
330 acaagagcag gtggcagcag gggAACGCTC tctcatgctc cgtgatgcat gaggtctgc 660  
331 acaaccacta cacgacaaag agcctctccc tgtctccggg taaatgatgt cgacggccgc 720  
332 gactctagag gat 733  
335 <210> SEQ ID NO: 5  
336 <211> LENGTH: 5  
337 <212> TYPE: PRT  
338 <213> ORGANISM: Homo sapiens  
340 <220> FEATURE:  
341 <221> NAME/KEY: SITE  
342 <222> LOCATION: (3)

→ Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
PATENT APPLICATION: US/10/078,059

DATE: 03/05/2002  
TIME: 14:12:04

Input Set : A:\PF466P2SEQLIST01102002.txt  
Output Set: N:\CRF3\03052002\J078059.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:560 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:610 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:722 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:835 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30